

FIGURE 1

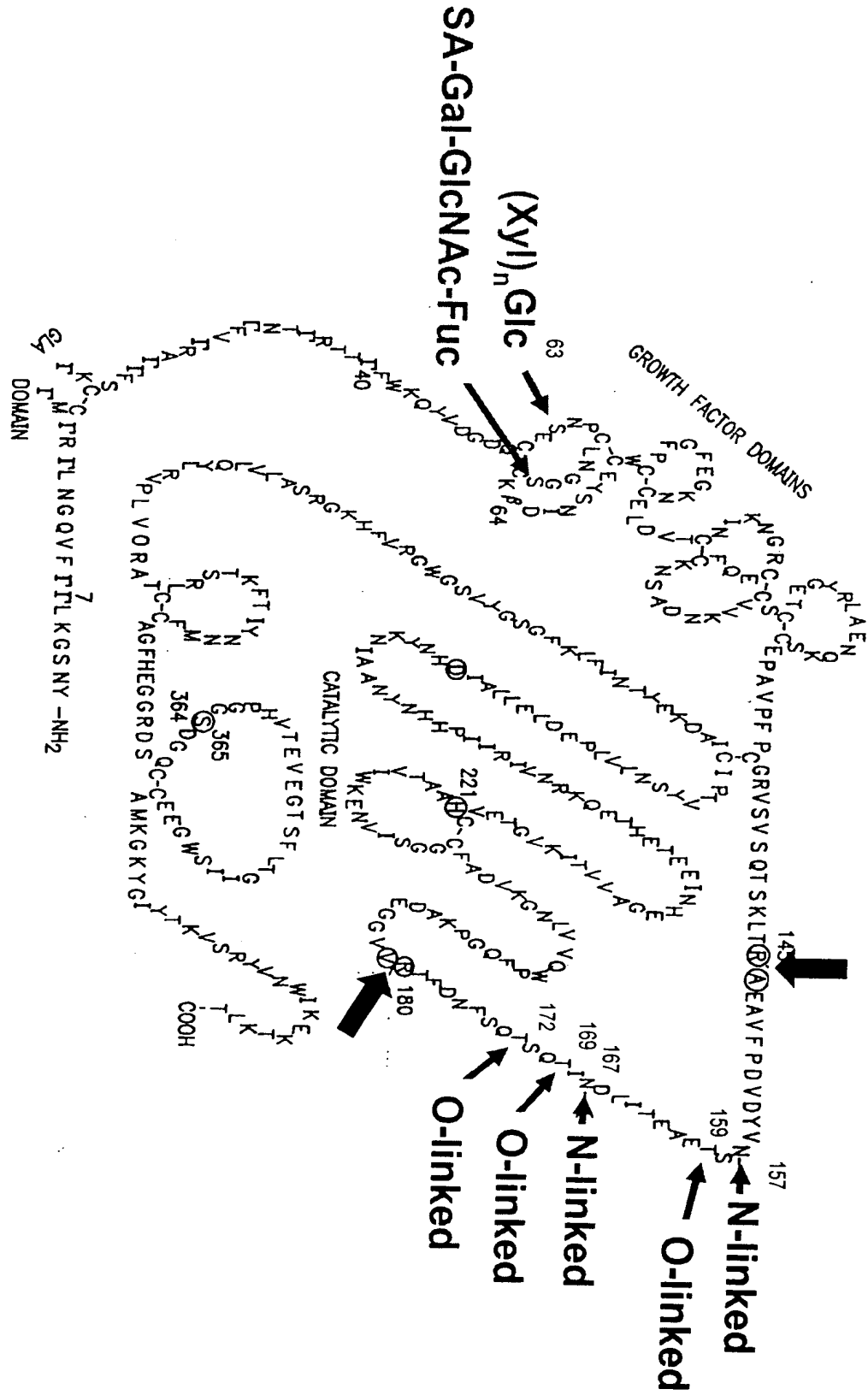


FIGURE 2A

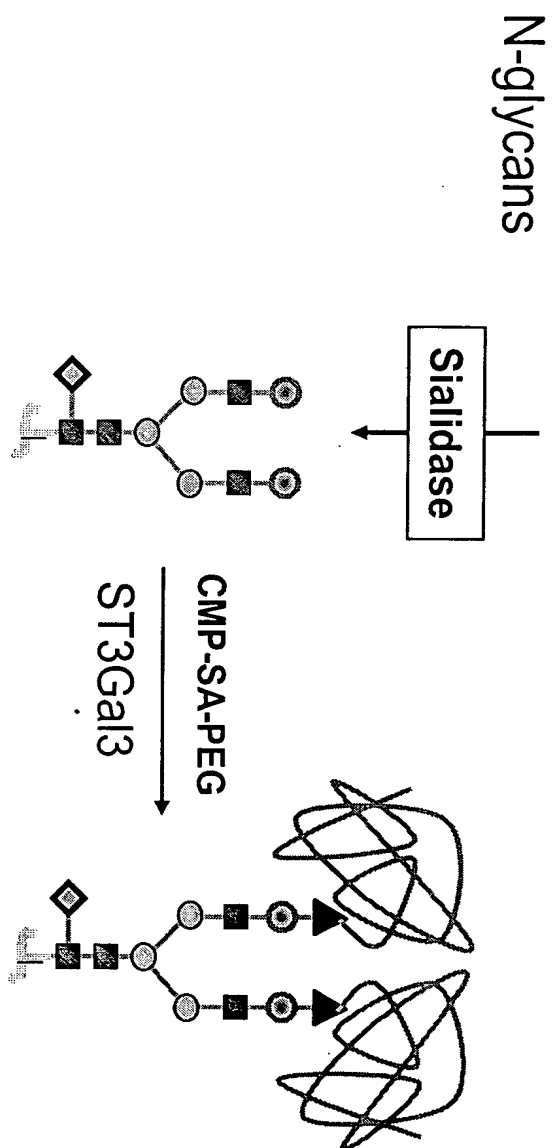


FIGURE 2B

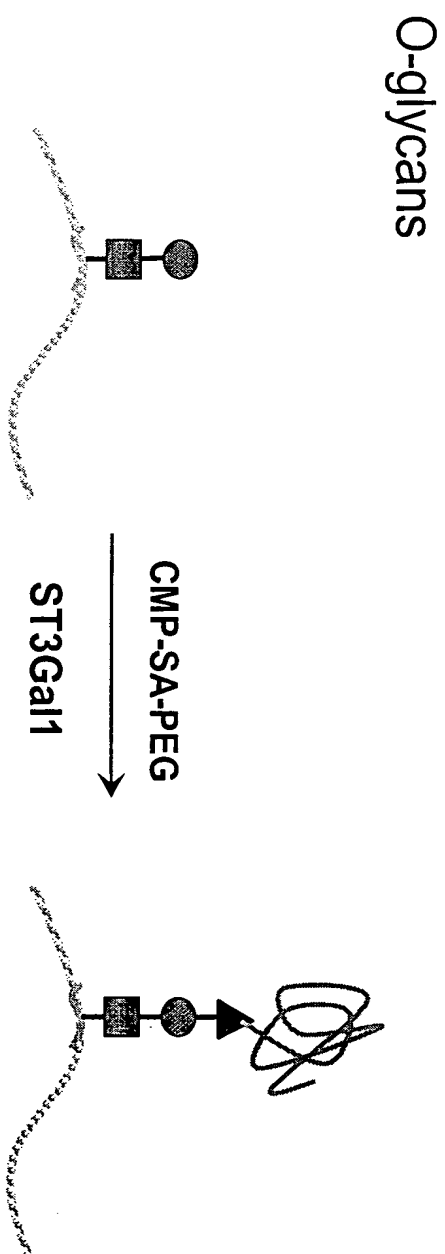


FIGURE 2C

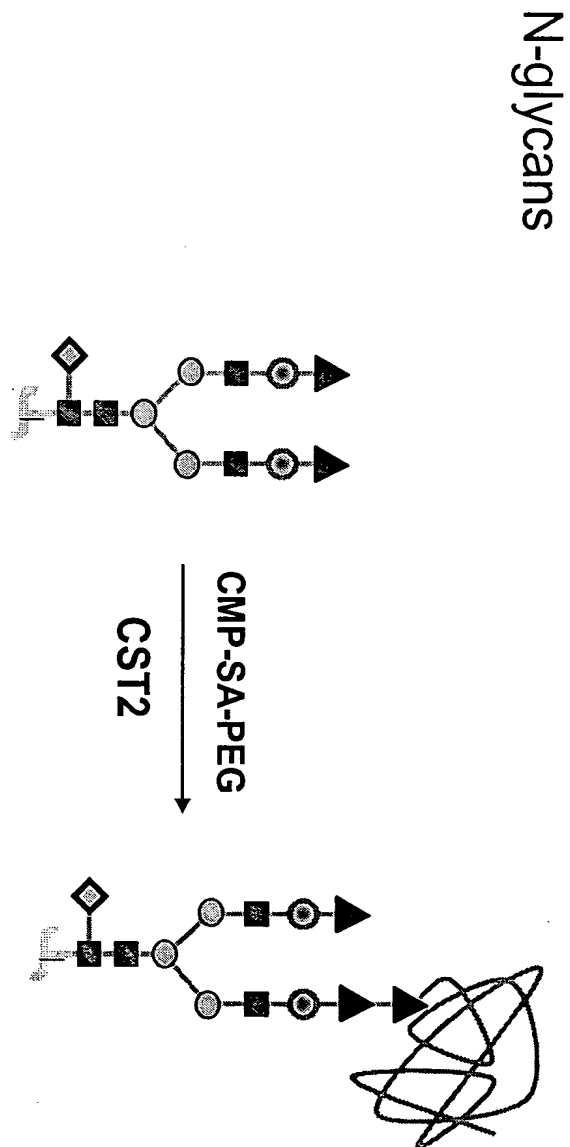


FIGURE 2D

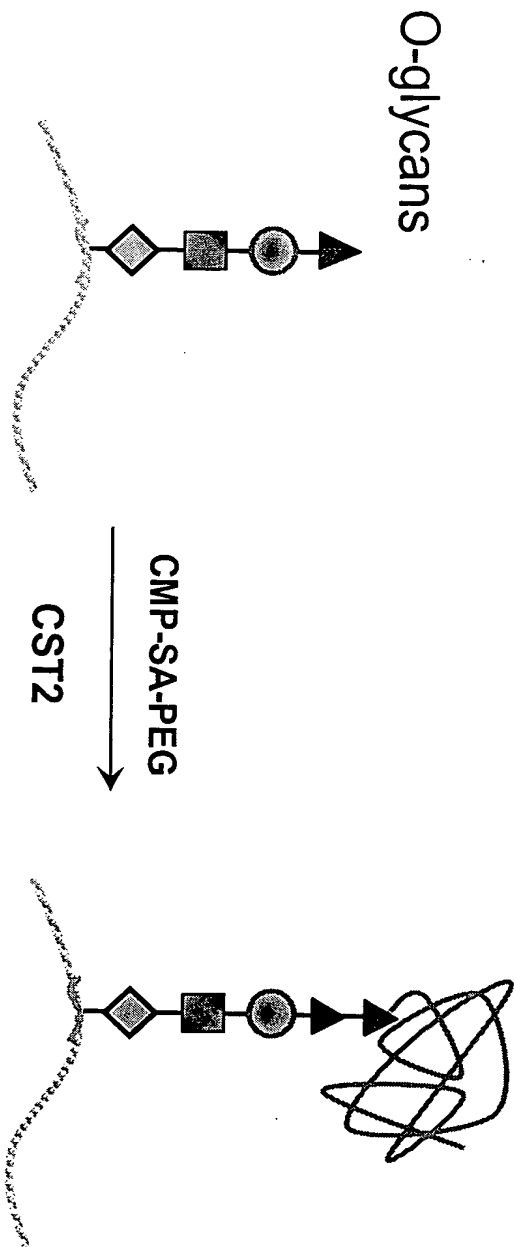
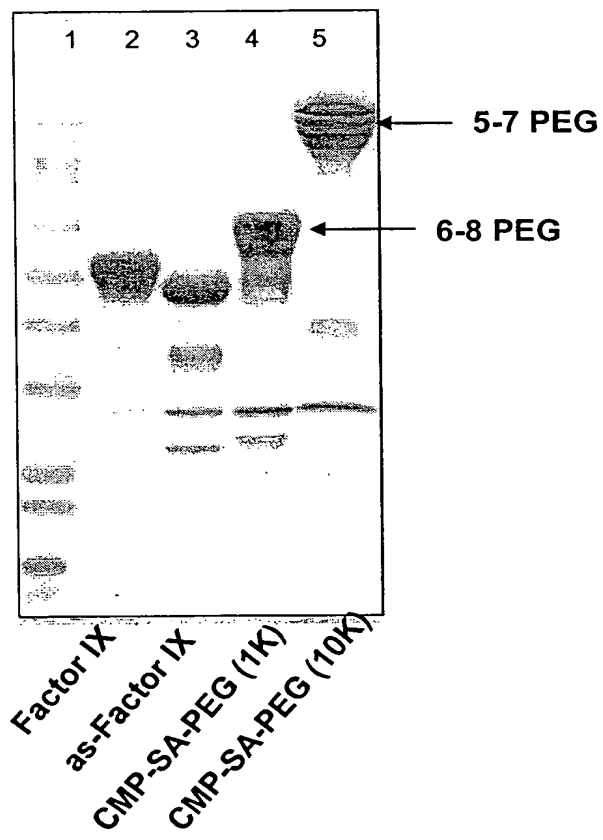


FIGURE 2E

Sialidase, ST3Gal3  
Reaction with CMP-  
SA-PEG (10 KDa)

4-20% SDS-PAGE gels

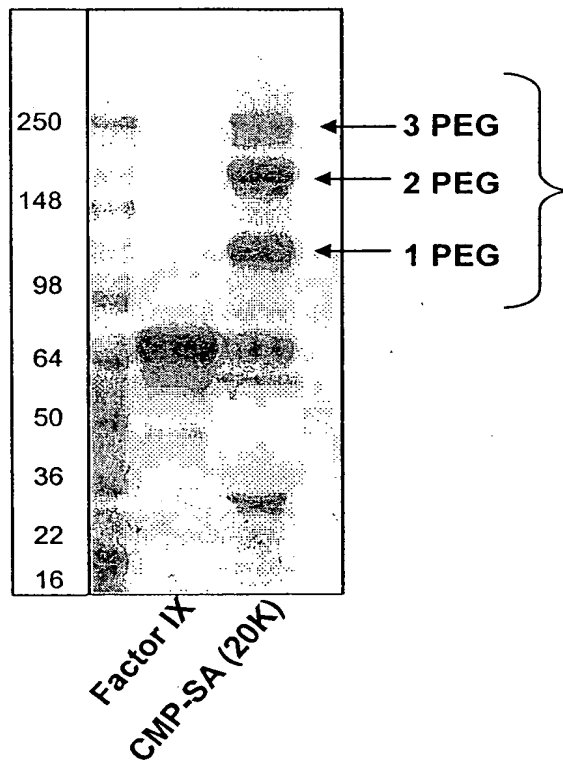


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FIGURE 2F

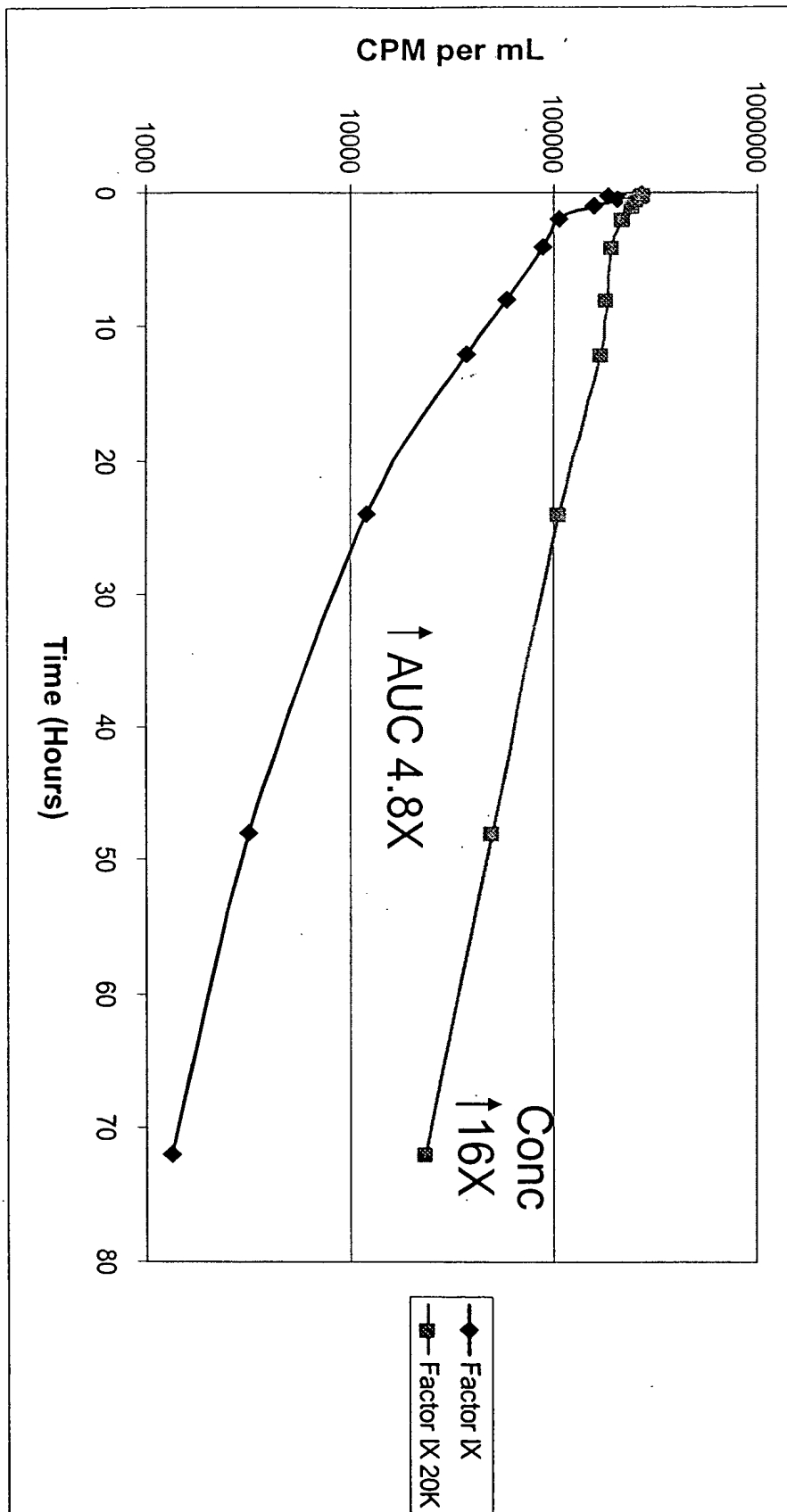
CST-II Reaction with  
CMP-SA-PEG (20 KDa)

4-12% SDS-PAGE gels



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FIGURE 3



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FIGURE 4

Enzyme	Specificity and Linkage	Reaction Conditions	PEG Incorporation (size)	Clotting Activity (Chromogenic Assay)
Factor IX (unmodified)	NA	NA	>90% sialylation	110-139%
ST3Gal3	N-linked glycans	CMP-SA	None. (incorporated 2-3% SA)	Full Activity
ST3Gal3	<i>N-linked glycans</i>	1. Sialidase 2. <i>CMP-SA-PEG (1 &amp; 10KDa)</i>	(1 K); 6-8 PEG (10 K); 5-7 PEG	PEG (1 KDa); 52%. PEG (10 KDa); 54%.
ST3Gal3	N-linked glycans	CMP-SA-PEG (10 KDa); no sialidase.	1-6 PEG (10 KDa);	1-2 PEG's (27 hrs); 164% ~3 PEG's (119 or 27 hrs); 97% 4-5 PEG's (119 hrs);
<b>CST-II</b> ( <i>Campylobacter</i> )		<i>CMP-SA-PEG (20 KDa); no sialidase</i>	<b>2-3 PEG (20 KDa)</b>	<b>96%</b>

## FIGURE 5

YNSGKLEEFVQGNLERECMEEKCSFEEAREVFENTERTTEFWKQYVDGDQ  
CESNPCLNGGSCCKDDINSYECWCPFGFEGKNCELDVTCNIKNGRCEQFCK  
NSADNKVVCSTEGYRLAENQKSCEPAVPFPCGRVSVSQTSKLTRA EAVFP  
DVDYVNSTEAEITLDNITQSTQSFNDFTRVVGGEDAKPGQFPWQVVLNGKV  
DAFCGGSIVNEKWIVTAAHCVETGVKITVVAGEHNIEETEHTEQKRN VIRIIPH  
HNYNAAINKYNHDIALLELDEPLVLNSYVTPICIADKEYTNIFLKFGSGYVSGWGRVFHK  
GRSALVLQYLRVPLVD RATCLRSTKFTIYNNMFCAGFHEGGRDSCQGDSGGPHVTEVE  
GTSFLTGIISWGEECAMKGKYG IYTKVSRYVNWIKEKTKLT

FIGURE 6

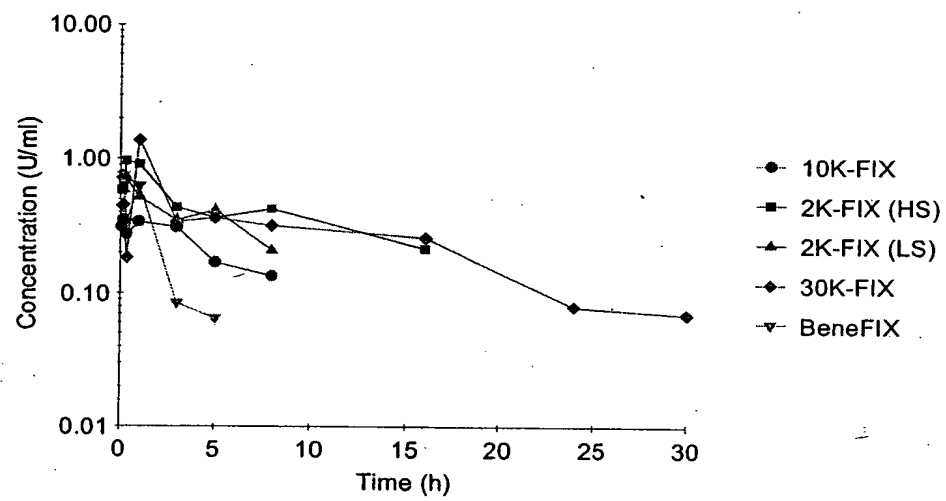


FIGURE 7  
FIGURE 7

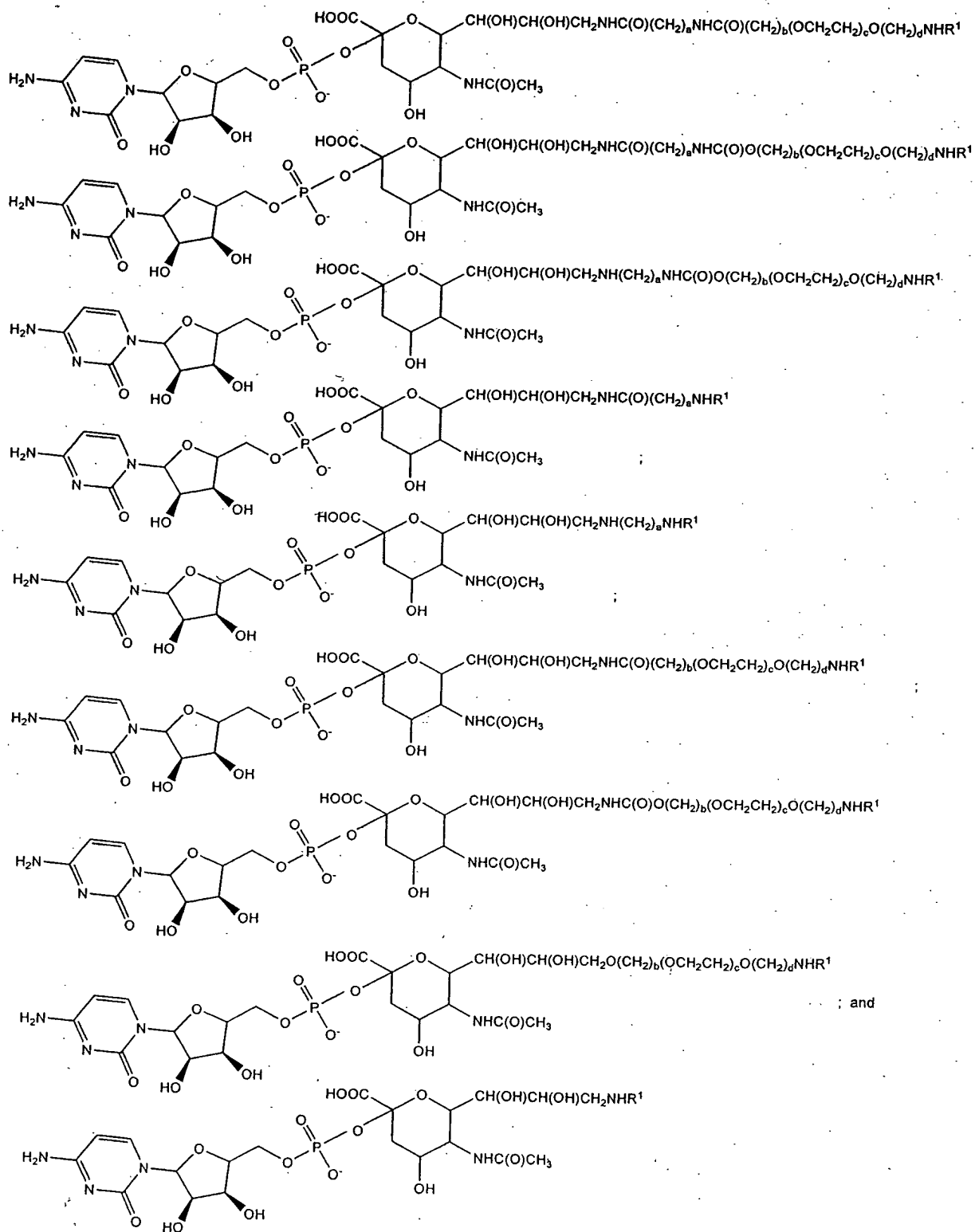


FIGURE 8

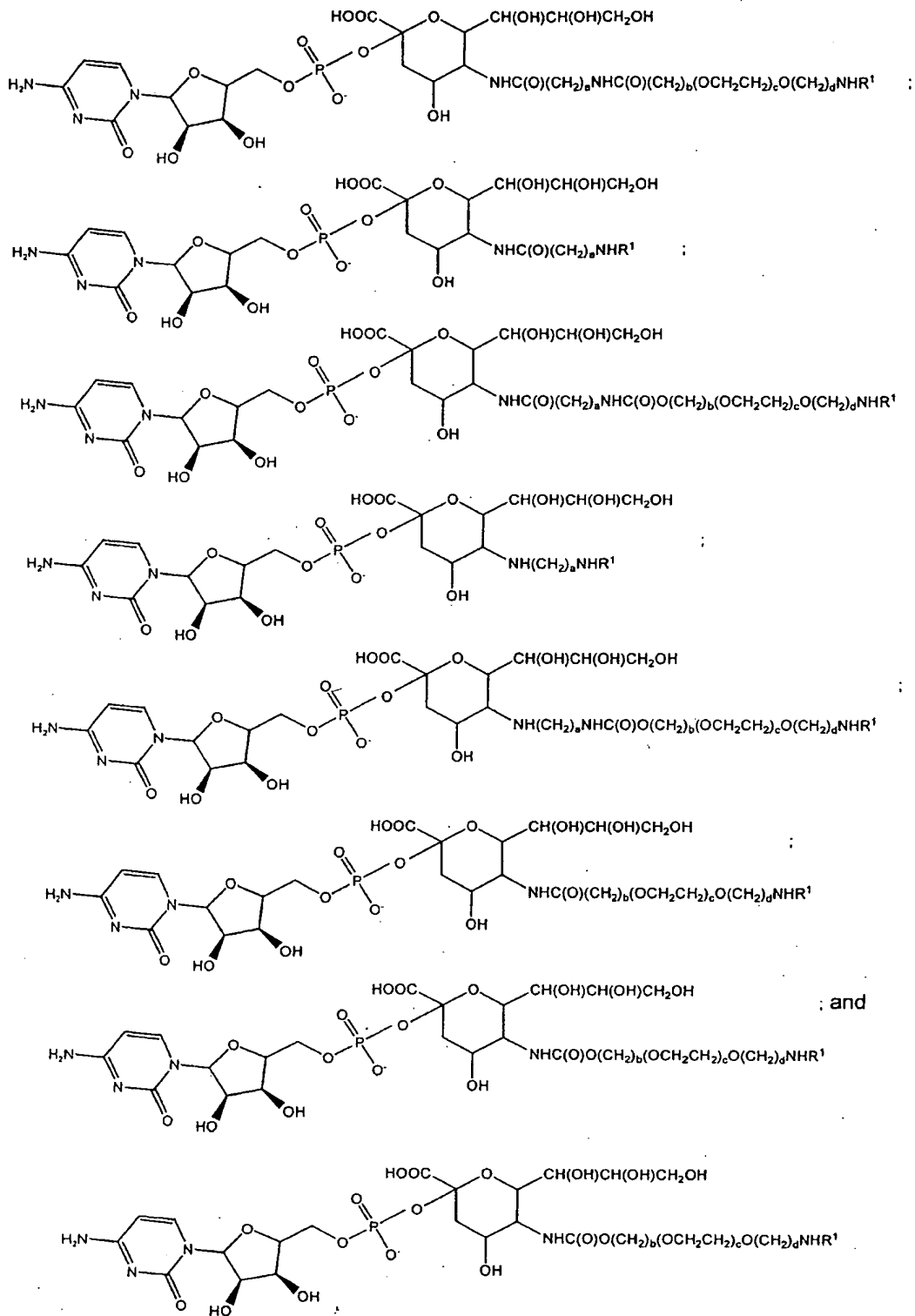


FIGURE 9A

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
At1g08280	<i>Arabidopsis thaliana</i>	n.d.	AC011438 BT004583 NC_003070	AAF18241.1 AAO42829.1 NP_172305.1	Q84W00 Q9SGD2
At1g08660/F22O13.14	<i>Arabidopsis thaliana</i>	n.d.	AC003981 AY064135 AY124807 NC_003070 NM_180609	AAF99778.1 AAL36042.1 AAM70516.1 NP_172342.1 NP_850940.1	Q8VZJ0 Q9FRR9
At3g48820/T21J18_90	<i>Arabidopsis thaliana</i>	n.d.	AY080589 AY133816 AL132963 NM_114741	AAL85966.1 AAM91750.1 CAB87910.1 NP_190451.1	Q8RY00 Q9M301
$\alpha$ -2,3-sialyltransferase (ST3Gal-IV)	<i>Bos taurus</i>	n.d.	AJ584673	CAE48298.1	
$\alpha$ -2,3-sialyltransferase (St3Gal-V)	<i>Bos taurus</i>	n.d.	AJ585768	CAE51392.1	
$\alpha$ -2,6-sialyltransferase (Siat7b)	<i>Bos taurus</i>	n.d.	AJ620651	CAF05850.1	
$\alpha$ -2,8-sialyltransferase (SIAT8A)	<i>Bos taurus</i>	2.4.99.8	AJ699418	CAG27880.1	
$\alpha$ -2,8-sialyltransferase (Siat8D)	<i>Bos taurus</i>	n.d.	AJ699421	CAG27883.1	
$\alpha$ -2,8-sialyltransferase ST8Sia-III (Siat8C)	<i>Bos taurus</i>	n.d.	AJ704563	CAG28696.1	
CMP $\alpha$ -2,6-sialyltransferase (ST6Gal I)	<i>Bos taurus</i>	2.4.99.1	Y15111 NM_177517	CAA75385.1 NP_803483.1	O18974
sialyltransferase 8 (fragment)	<i>Bos taurus</i>	n.d.	AF450088	AAL47018.1	Q8WN13
sialyltransferase ST3Gal-II (Siat4B)	<i>Bos taurus</i>	n.d.	AJ748841	CAG44450.1	
sialyltransferase ST3Gal-III (Siat6)	<i>Bos taurus</i>	n.d.	AJ748842	CAG44451.1	
sialyltransferase ST3Gal-VI (Siat10)	<i>Bos taurus</i>	n.d.	AJ748843	CAG44452.1	
ST3Gal I	<i>Bos taurus</i>	n.d.	AJ305086	CAC24698.1	Q9BEG4
St6GalNAc-VI	<i>Bos taurus</i>	n.d.	AJ620949	CAF06586.1	
CDS4	<i>Branchiostoma floridae</i>	n.d.	AF391289	AAM18873.1	Q8T771
polysialyltransferase (PST) (fragment) ST8Sia IV	<i>Cercopithecus aethiops</i>	2.4.99.-	AF210729	AAF17105.1	Q9TT09
polysialyltransferase (STX) (fragment) ST8Sia II	<i>Cercopithecus aethiops</i>	2.4.99.-	AF210318	AAF17104.1	Q9TT10
$\alpha$ -2,3-sialyltransferase ST3Gal I (Siat4)	<i>Ciona intestinalis</i>	n.d.	AJ626815	CAF25173.1	
$\alpha$ -2,3-sialyltransferase ST3Gal I (Siat4)	<i>Ciona savignyi</i>	n.d.	AJ626814	CAF25172.1	
$\alpha$ -2,8-polysialyltransferase ST8Sia IV	<i>Cricetulus griseus</i>	2.4.99.-	- Z46801	AAE28634 CAA86822.1	Q64690
Gal $\beta$ 1,3/4-GlcNAc $\alpha$ -2,3-sialyltransferase St3Gal I	<i>Cricetulus griseus</i>	n.d.	AY266675	AAP22942.1	Q80WLO
Gal $\beta$ 1,3/4-GlcNAc $\alpha$ -2,3-sialyltransferase St3Gal II (fragment)	<i>Cricetulus griseus</i>	n.d.	AY266676	AAP22943.1	Q80WK9
$\alpha$ -2,3-sialyltransferase ST3Gal I (Siat4)	<i>Danio rerio</i>	n.d.	AJ783740	CAH04017.1	
$\alpha$ -2,3-sialyltransferase ST3Gal II (Siat5)	<i>Danio rerio</i>	n.d.	AJ783741	CAH04018.1	

FIGURE 9B

Protein	Organism	EC#	GenBank / GenPept		SwissProt	PDB / 3D
$\alpha$ -2,3-sialyltransferase ST3Gal III (Siat6)	<i>Danio rerio</i>	n.d.	AJ626821	CAF25179.1		
$\alpha$ -2,3-sialyltransferase ST3Gal IV (Siat4c)	<i>Danio rerio</i>	n.d.	AJ744809	CAG32845.1		
$\alpha$ -2,3-sialyltransferase ST3Gal V-r (Siat5-related)	<i>Danio rerio</i>	n.d.	AJ783742	CAH04019.1		
$\alpha$ -2,6-sialyltransferase ST6Gal I (Siat1)	<i>Danio rerio</i>	n.d.	AJ744801	CAG32837.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc II (Siat7B)	<i>Danio rerio</i>	n.d.	AJ634459	CAG25680.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc V (Siat7E) (fragment)	<i>Danio rerio</i>	n.d.	AJ646874	CAG26703.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc VI (Siat7F) (fragment)	<i>Danio rerio</i>	n.d.	AJ646883	CAG26712.1		
$\alpha$ -2,8-sialyltransferase ST8Sia I (Siat 8A) (fragment)	<i>Danio rerio</i>	n.d.	AJ715535	CAG29374.1		
$\alpha$ -2,8-sialyltransferase ST8Sia III (Siat 8C) (fragment)	<i>Danio rerio</i>	n.d.	AJ715543	CAG29382.1		
$\alpha$ -2,8-sialyltransferase ST8Sia IV (Siat 8D) (fragment)	<i>Danio rerio</i>	n.d.	AJ715545	CAG29384.1		
$\alpha$ -2,8-sialyltransferase ST8Sia V (Siat 8E) (fragment)	<i>Danio rerio</i>	n.d.	AJ715546	CAG29385.1		
$\alpha$ -2,8-sialyltransferase ST8Sia VI (Siat 8F) (fragment)	<i>Danio rerio</i>	n.d.	AJ715551	CAG29390.1		
$\beta$ -galactosamide $\alpha$ -2,6-sialyltransferase II (ST6Gal II)	<i>Danio rerio</i>	n.d.	AJ627627	CAF29495.1		
N-glycan $\alpha$ -2,8-sialyltransferase	<i>Danio rerio</i>	n.d.	BC050483 AY055462 NM_153662	AAH50483.1 AAL17875.1 NP_705948.1	Q7ZU51 Q8QH83	
ST3Gal III-related (sial6r)	<i>Danio rerio</i>	n.d.	BC053179 AJ626820 NM_200355	AAH53179.1 CAF25178.1 NP_956649.1	Q7T3B9	
St3Gal-V	<i>Danio rerio</i>	n.d.	AJ619960	CAF04061.1		
st6GalNAc-VI	<i>Danio rerio</i>	n.d.	BC060932 AJ620947	AAH60932.1 CAF06584.1		
$\alpha$ -2,6-sialyltransferase (CG4871) ST6Gal I	<i>Drosophila melanogaster</i>	2.4.99.1	AE003465 AF218237 AF397532 AE003465 NM_079129 NM_166684	AAF47256.1 AAG13185.1 AAK92126.1 AAM70791.1 NP_523853.1 NP_726474.1	Q9GU23 Q9W121	
$\alpha$ -2,3-sialyltransferase (ST3Gal-VI)	<i>Gallus gallus</i>	n.d.	AJ585767 AJ627204	CAE51391.1 CAF25503.1		
$\alpha$ -2,3-sialyltransferase ST3Gal I	<i>Gallus gallus</i>	2.4.99.4	X80503 NM_205217	CAA56666.1 NP_990548.1	Q11200	
$\alpha$ -2,3-sialyltransferase ST3Gal IV (fragment)	<i>Gallus gallus</i>	2.4.99.-	AF035250	AAC14163.1	O73724	
$\alpha$ -2,3-sialyltransferase (ST3GAL-II)	<i>Gallus gallus</i>	n.d.	AJ585761	CAE51385.2		
$\alpha$ -2,6-sialyltransferase (Siat7b)	<i>Gallus gallus</i>	n.d.	AJ620653	CAF05852.1		
$\alpha$ -2,6-sialyltransferase ST6Gal I	<i>Gallus gallus</i>	2.4.99.1	X75558 NM_205241	CAA53235.1 NP_990572.1	Q92182	
$\alpha$ -2,6-sialyltransferase	<i>Gallus gallus</i>	2.4.99.3	-	AAE68028.1	Q92183	

FIGURE 9C

Protein	Organism	EC#	GenBank / GenPept		SwissProt	PDB / 3D
ST6GalNAc I			-	AAE68029.1 X74946 CAA52902.1 NM_205240 NP_990571.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc II	<i>Gallus gallus</i>	2.4.99.-	X77775 NM_205233	AAE68030.1 CAA54813.1 NP_990564.1	Q92184	
$\alpha$ -2,6-sialyltransferase ST6GalNAc III (SIAT7C) (fragment)	<i>Gallus gallus</i>	n.d.	AJ634455	CAG25677.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc V (SIAT7E) (fragment)	<i>Gallus gallus</i>	n.d.	AJ646877	CAG26706.1		
$\alpha$ -2,8-sialyltransferase (GD3 Synthase) ST8Sia I	<i>Gallus gallus</i>	2.4.99.-	U73176	AAC28888.1	P79783	
$\alpha$ -2,8-sialyltransferase (SIAT8B)	<i>Gallus gallus</i>	n.d.	AJ699419	CAG27881.1		
$\alpha$ -2,8-sialyltransferase (SIAT8C)	<i>Gallus gallus</i>	n.d.	AJ699420	CAG27882.1		
$\alpha$ -2,8-sialyltransferase (SIAT8F)	<i>Gallus gallus</i>	n.d.	AJ699424	CAG27886.1		
$\alpha$ -2,8-sialyltransferase ST8Sia-V (SIAT8C)	<i>Gallus gallus</i>	n.d.	AJ704564	CAG28697.1		
$\beta$ -galactosamide $\alpha$ -2,6- sialyltransferase II (ST6Gal II)	<i>Gallus gallus</i>	n.d.	AJ627629	CAF29497.1		
GM3 synthase (SIAT9)	<i>Gallus gallus</i>	2.4.99.9	AY515255	AAS83519.1		
polysialyltransferase ST8Sia IV	<i>Gallus gallus</i>	2.4.99.-	AF008194	AAB95120.1	O42399	
$\alpha$ -2,3-sialyltransferase ST3Gal I	<i>Homo sapiens</i>	2.4.99.4	L29555 AF059321 L13972 AF155238 AF186191 BC018357 NM_003033 NM_173344	AAA36612.1 AAC17874.1 AAC37574.1 AAD39238.1 AAG29876.1 AAH18357.1 NP_003024.1 NP_775479.1	Q11201 O60677 Q9UN51	
$\alpha$ -2,3-sialyltransferase ST3Gal II	<i>Homo sapiens</i>	2.4.99.4	U63090 BC036777 X96667 NM_006927	AAB40389.1 AAH36777.1 CAA65447.1 NP_008858.1	Q16842 O00654	
$\alpha$ -2,3-sialyltransferase ST3Gal III (SiaT6)	<i>Homo sapiens</i>	2.4.99.6	L23768 BC050380 AF425851 AF425852 AF425853 AF425854 AF425855 AF425856 AF425857 AF425858 AF425859 AF425860 AF425861 AF425862 AF425863 AF425864 AF425865 AF425866 AF425867 AY167992 AY167993 AY167994	AAA35778.1 AAH50380.1 AAO13859.1 AAO13860.1 AAO13861.1 AAO13862.1 AAO13863.1 AAO13864.1 AAO13865.1 AAO13866.1 AAO13867.1 AAO13868.1 AAO13869.1 AAO13870.1 AAO13871.1 AAO13872.1 AAO13873.1 AAO13874.1 AAO13875.1 AAO38806.1 AAO38807.1 AAO38808.1	Q11203 Q86UR6 Q86UR7 Q86UR8 Q86UR9 Q86US0 Q86US1 Q86US2 Q8IX43 Q8IX44 Q8IX45 Q8IX46 Q8IX47 Q8IX48 Q8IX49 Q8IX50 Q8IX51 Q8IX52 Q8IX53 Q8IX54 Q8IX55 Q8IX56	

FIGURE 9D

Protein	Organism		EC#	GenBank / GenPept		SwissProt	PDB / 3D
				AY167995 AY167996 AY167997 AY167998 NM_006279 NM_174964 NM_174965 NM_174966 NM_174967 NM_174969 NM_174970 NM_174972	AAO38809.1 AAO38810.1 AAO38811.1 AAO38812.1 NP_006270.1 NP_777624.1 NP_777625.1 NP_777626.1 NP_777627.1 NP_777629.1 NP_777630.1 NP_777632.1	Q8IX57 Q8IX58	
$\alpha$ -2,3-sialyltransferase ST3Gal IV		<i>Homo sapiens</i>	2.4.99.-	L23767 AF035249 BC010645 AY040826 AF516602 AF516603 AF516604 AF525084 X74570 CR456858 NM_006278	AAA16460.1 AAC14162.1 AAH10645.1 AAK93790.1 AAM66431.1 AAM66432.1 AAM66433.1 AAM81378.1 CAA52662.1 CAG33139.1 NP_006269.1	Q11206 O60497 Q96QQ9 Q8N6A6 Q8N6A7 Q8NFD3 Q8NFG7	
$\alpha$ -2,3-sialyltransferase ST3Gal VI		<i>Homo sapiens</i>	2.4.99.4	AF119391 BC023312 AB022918 AX877828 AX886023 NM_006100	AAD39131.1 AAH23312.1 BAA77609.1 CAE89895.1 CAF00161.1 NP_006091.1	Q9Y274	
$\alpha$ -2,6-sialyltransferase (ST6Gal II ; KIAA1877)		<i>Homo sapiens</i>	n.d.	BC008680 AB058780 AB059555 AJ512141 AX795193 AX795193 NM_032528	AAH08680.1 BAB47506.1 BAC24793.1 CAD54408.1 CAE48260.1 CAE48261.1 NP_115917.1	Q86Y44 Q8IUG7 Q96HE4 Q96JF0	
$\alpha$ -2,6-sialyltransferase (ST6GALNAC III)		<i>Homo sapiens</i>	n.d.	BC059363 AY358540 AK091215 AJ507291 NM_152996	AAH59363.1 AAQ88904.1 BAC03611.1 CAD45371.1 NP_694541.1	Q8N259 Q8NDV1	
$\alpha$ -2,6-sialyltransferase (ST6GalNAc V)		<i>Homo sapiens</i>	n.d.	BC001201 AK056241 AL035409 AJ507292 NM_030965	AAH01201.1 BAB71127.1 CAB72344.1 CAD45372.1 NP_112227.1	Q9BVH7	
$\alpha$ -2,6-sialyltransferase (SThM) ST6GalNAc II		<i>Homo sapiens</i>	2.4.99.-	U14550 BC040455 AJ251053 NM_006456	AAA52228.1 AAH40455.1 CAB61434.1 NP_006447.1	Q9UJ37 Q12971	
$\alpha$ -2,6-sialyltransferase ST6Gal I		<i>Homo sapiens</i>	2.4.99.1	BC031476 BC040009 A17362 A23699 X17247 X54363 X62822 NM_003032 NM_173216	AAH31476.1 AAH40009.1 CAA01327.1 CAA01686.1 CAA35111.1 CAA38246.1 CAA44634.1 NP_003023.1 NP_775323.1	P15907	
$\alpha$ -2,6-sialyltransferase ST6GalNAc I		<i>Homo sapiens</i>	2.4.99.3	BC022462 AY096001 AY358918 AK000113 Y11339	AAH22462.1 AAM22800.1 AAQ89277.1 BAA90953.1 CAA72179.2	Q8TBJ6 Q9NSC7 Q9NXQ7	

FIGURE 9E

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
			NM_018414 NP_060884.1		
$\alpha$ -2,8-polysialyltransferase ST8Sia IV	<i>Homo sapiens</i>	2.4.99.-	L41680 AAC41775.1 BC027866 AAH27866.1 BC053657 AAH53657.1 NM_005668 NP_005659.1	Q8N1F4 Q92187 Q92693	
$\alpha$ -2,8-sialyltransferase (GD3 synthase) ST8Sia I	<i>Homo sapiens</i>	2.4.99.8	L32867 AAA62366.1 L43494 AAC37586.1 BC046158 AAH46158.1 - AAQ53140.1 AY569975 AAS75783.1 D26360 BAA05391.1 X77922 CAA54891.1 NM_003034 NP_003025.1	Q86X71 Q92185 Q93064	
$\alpha$ -2,8-sialyltransferase ST8Sia II	<i>Homo sapiens</i>	2.4.99.-	L29556 AAA36613.1 U82762 AAB51242.1 U33551 AAC24458.1 BC069584 AAH69584.1 NM_006011 NP_006002.1	Q92186 Q92470 Q92746	
$\alpha$ -2,8-sialyltransferase ST8Sia III	<i>Homo sapiens</i>	2.4.99.-	AF004668 AAB87642.1 AF003092 AAC15901.2 NM_015879 NP_056963.1	O43173 Q9NS41	
$\alpha$ -2,8-sialyltransferase ST8Sia V	<i>Homo sapiens</i>	2.4.99.-	U91641 AAC51727.1 CR457037 CAG33318.1 NM_013305 NP_037437.1	O15466	
ENSP00000020221 (fragment)		n.d.	AC023295 -		
lactosylceramide $\alpha$ -2,3-sialyltransferase (ST3Gal V)	<i>Homo sapiens</i>	2.4.99.9	AF105026 AAD14634.1 AF119415 AAF66146.1 BC065936 AAH65936.1 AY152815 AAO16866.1 AAP65066 AAP65066.1 AY359105 AAQ89463.1 AB018356 BAA33950.1 AX876536 CAE89320.1 NM_003896 NP_003887.2	Q9UNP4 O94902	
<i>N</i> -acetylgalactosaminide $\alpha$ -2,6-sialyltransferase (ST6GalNAc VI)	<i>Homo sapiens</i>	2.4.99.-	BC006564 AAH06564.1 BC007802 AAH07802.1 BC016299 AAH16299.1 AY358672 AAQ89035.1 AB035173 BAA87035.1 AK023900 BAB14715.1 AJ507293 CAD45373.1 AX880950 CAE91145.1 CR457318 CAG33599.1 NM_013443 NP_038471.2	Q969X2 Q9H8A2 Q9ULB8	
<i>N</i> -acetylgalactosaminide $\alpha$ -2,6-sialyltransferase IV (ST6GalNAc IV)	<i>Homo sapiens</i>	2.4.99.-	AF127142 AAF00102.1 BC036705 AAH36705.1 - AAP63349.1 AB035172 BAA87034.1 AK000600 BAA91281.1 Y17461 CAB44354.1 AJ271734 CAC07404.1 AX061620 CAC24981.1 AX068265 CAC27250.1 AX969252 CAF14360.1 NM_014403 NP_055218.3 NM_175039 NP_778204.1	Q9H4F1 Q9NWU6 Q9UKU1 Q9ULB9 Q9Y3G3 Q9Y3G4	
ST8SIA-VI (fragment)	<i>Homo sapiens</i>	n.d.	AJ621583 CAF21722.1 XM_291725 XP_291725.2		
unnamed protein product	<i>Homo sapiens</i>	n.d.	AK021929 BAB13940.1 AX881696 CAE91353.1	Q9HAA9	
Gal $\beta$ -1,3/4-GlcNAc $\alpha$ -	<i>Mesocricetus</i>	2.4.99.6	AJ245699 CAB53394.1	Q9QXF6	

FIGURE 9F

Protein	Organism	EC#	GenBank / GenPept		SwissProt	PDB / 3D
2,3-sialyltransferase (ST3Gal III)	<i>auratus</i>					
Gal $\beta$ 1,3/4-GlcNAc $\alpha$ -2,3-sialyltransferase (ST3Gal IV)	<i>Mesocricetus auratus</i>	2.4.99.6	AJ245700	CAB53395.1	Q9QXF5	
GD3 synthase (fragment) ST8Sia I	<i>Mesocricetus auratus</i>	n.d.	AF141657	AAD33879.1	Q9WUL1	
polysialyltransferase (ST8Sia IV)	<i>Mesocricetus auratus</i>	2.4.99.-	AJ245701	CAB53396.1	Q9QXF4	
$\alpha$ -2,3-sialyltransferase ST3Gal I	<i>St3gal1</i> <i>Mus musculus</i>	2.4.99.4	AF214028 AK031344 AK078469 X73523 NM_009177	AAF60973.1 BAC27356.1 BAC37290.1 CAA51919.1 NP_033203.1	P54751 Q11202 Q9JL30	
$\alpha$ -2,3-sialyltransferase ST3Gal II	<i>St3gal2</i> <i>Mus musculus</i>	2.4.99.4	BC015264 BC066064 AK034554 AK034863 AK053827 X76989 NM_009179 NM_178048	AAH15264.1 AAH66064.1 BAC28752.1 BAC28859.1 BAC35543.1 CAA54294.1 NP_033205.1 NP_835149.1	Q11204 Q8BPL0 Q8BSA0 Q8BSE9 Q91WH6	
$\alpha$ -2,3-sialyltransferase ST3Gal III	<i>St3gal3</i> <i>Mus musculus</i>	2.4.99.-	BC006710 AK005053 AK013016 X84234 NM_009176	AAH06710.1 BAB23779.1 BAB28598.1 CAA59013.1 NP_033202.2	P97325 Q922X5 Q9CZ48 Q9DBB6	
$\alpha$ -2,3-sialyltransferase ST3Gal IV	<i>St3gal4</i> <i>Mus musculus</i>	2.4.99.4	BC011121 BC050773 D28941 AK008543 AB061305 X95809 NM_009178	AAH11121.1 AAH50773.1 BAA06068.1 BAB25732.1 BAB47508.1 CAA65076.1 NP_033204.2	P97354 Q61325 Q91Y74 Q921R5 Q9CVE8	
$\alpha$ -2,3-sialyltransferase ST3Gal VI	<i>St3gal6</i> <i>Mus musculus</i>	2.4.99.4	AF119390 BC052338 AB063326 AK033562 AK041173 NM_018784	AAD39130.1 AAH52338.1 BAB79494.1 BAC28360.1 BAC30851.1 NP_061254	Q80UR7 Q8BLV1 Q8VIB3 Q9WVG2	
$\alpha$ -2,6-sialyltransferase ST6GalNAc II	<i>St6galnac2</i> <i>Mus musculus</i>	2.4.99.-	NM_009180 BC010208 AB027198 AK004613 X93999 X94000 NM_009180	6677963 AAH10208.1 BAB00637.1 BAB23410.1 CAA63821.1 CAA63822.1 NP_033206.2	P70277 Q9DC24 Q9JIM5	
$\alpha$ -2,6-sialyltransferase ST6Gal I	<i>St6gal1</i> <i>Mus musculus</i>	2.4.99.1	- BC027833 D16106 AK034768 AK084124 NM_145933	AAE68031.1 AAH27833.1 BAA03680.1 BAC28828.1 BAC39120.1 NP_666045.1	Q64685 Q8BM62 Q8K1L1	
$\alpha$ -2,6-sialyltransferase ST6Gal II	<i>St6gal2</i> <i>Mus musculus</i>	n.d.	AK082566 AB095093 AK129462 NM_172829	BAC38534.1 BAC87752.1 BAC98272.1 NP_766417.1	Q8BUU4	
$\alpha$ -2,6-sialyltransferase ST6GalNAc I	<i>St6galnac1</i> <i>Mus musculus</i>	2.4.99.3	Y11274 NM_011371	CAA72137.1 NP_035501.1	Q9QZ39 Q9JJP5	
$\alpha$ -2,6-sialyltransferase ST6GalNAc III	<i>St6galnac3</i> <i>Mus musculus</i>	n.d.	BC058387 AK034804 Y11342 Y11343	AAH58387.1 BAC28836.1 CAA72181.2 CAB95031.1	Q9WUV2 Q9JHP5	

FIGURE 9G

Protein	Organism		EC#	GenBank / GenPept		SwissProt	PDB / 3D
				NM_011372	NP_035502		
$\alpha$ -2,6-sialyltransferase ST6GalNAc IV	<i>St6galnac4</i>	<i>Mus musculus</i>	2.4.99.7	BC056451 AK085730 AJ007310 Y15779 Y15780 Y19055 Y19057 NM_011373	AAH56451.1 BAC39523.1 CAA07446.1 CAB43507.1 <b>CAB43514.1</b> CAB93946.1 CAB93948.1 NP_035503.1	Q8C3J2 Q9JHP2 Q9R2B6 Q88725 Q9JHP0 Q9QUP9 Q9R2B5	
$\alpha$ -2,8-sialyltransferase (GD3 synthase) ST8Sia I	<i>St8sia1</i>	<i>Mus musculus</i>	2.4.99.8	L38677 BC024821 AK046188 AK052444 X84235 AJ401102 NM_011374	AAH91869.1 <b>AAH24821.1</b> BAC32625.1 BAC34994.1 CAA59014.1 CAC20706.1 NP_035504.1	Q64468 Q64687 Q8BL76 Q8BWIO Q8K1C1 Q9EPK0	
$\alpha$ -2,8-sialyltransferase (ST8Sia VI)	<i>St8sia6</i>	<i>Mus musculus</i>	n.d.	AB059554 AK085105 NM_145838	<b>BAC01265.1</b> BAC39367.1 NP_665837.1	Q8BI43 Q8K4T1	
$\alpha$ -2,8-sialyltransferase ST8Sia II	<i>St8sia2</i>	<i>Mus musculus</i>	2.4.99.-	X83562 X99646 X99647 X99648 X99649 X99650 X99651 NM_009181	CAA58548.1 CAA67965.1 CAA67965.1 CAA67965.1 CAA67965.1 CAA67965.1 CAA67965.1 NP_033207.1	<b>O35696</b>	
$\alpha$ -2,8-sialyltransferase ST8Sia IV	<i>St8sia4</i>	<i>Mus musculus</i>	2.4.99.8	BC060112 AK003690 AK041723 AJ223956 X86000 Y09484 NM_009183	AAH60112.1 BAB22941.1 BAC31044.1 <b>CAA11685.1</b> CAA59992.1 CAA70692.1 NP_033209.1	Q64692 Q8BY70	
$\alpha$ -2,8-sialyltransferase ST8Sia V	<i>St8sia5</i>	<i>Mus musculus</i>	2.4.99.-	BC034855 AK078670 X98014 X98014 X98014 NM_013666 NM_153124 NM_177416	AAH34855.1 BAC37354.1 <b>CAA66642.1</b> CAA66643.1 CAA66644.1 NP_038694.1 NP_694764.1 NP_803135.1	P70126 P70127 P70128 Q8BJW0 Q8JZQ3	
$\alpha$ -2,8-sialyltransferase ST8Sia III	<i>St8sia3</i>	<i>Mus musculus</i>	2.4.99.-	BC075645 AK015874 X80502 NM_009182	AAH75645.1 BAB30012.1 CAA56665.1 NP_033208.1	<b>Q64689</b> Q9CUJ6	
GD1 synthase (ST6GalNAc V)	<i>St6galnac5</i>	<i>Mus musculus</i>	n.d.	BC055737 AB030836 AB028840 AK034387 AK038434 AK042683 NM_012028	<b>AAH55737.1</b> BAA85747.1 BAA89292.1 BAC28693.1 BAC29997.1 BAC31331.1 NP_036158.2	Q8CAM7 Q8CBX1 Q9QYJ1 Q9R0K6	
GM3 synthase ( $\alpha$ -2,3-sialyltransferase) ST3Gal V	<i>St3gal5</i>	<i>Mus musculus</i>	2.4.99.9	AF119416 - AB018048 AB013302 AK012961 Y15003 NM_011375	<b>AAF66147.1</b> AAP65063.1 BAA33491.1 BAA76467.1 BAB28571.1 CAA75235.1 NP_035505.1	Q88829 Q9CZ65 Q9QWF9	
N-acetylgalactosaminide $\alpha$ -2,6-sialyltransferase (ST6GalNAc VI)	<i>St6galnac6</i>	<i>Mus musculus</i>	2.4.99.-	BC036985 AB035174 AB035123 AK030648	<b>AAH36985.1</b> BAA87036.1 BAA95940.1 BAC27064.1	Q8CDC3 Q8JZW3 Q9JM95 Q9R0G9	

FIGURE 9H

Protein	Organism	EC#	GenBank / GenPept		SwissProt	PDB / 3D
			NM_016973	NP_058669.1		
M138L	<i>Myxoma virus</i>	n.d.	U46578 AF170726 NC_001132	AAD00069.1 AAE61323.1 AAE61326.1 AAF15026.1 NP_051852.1		
$\alpha$ -2,3-sialyltransferase (St3Gal-I)	<i>Oncorhynchus mykiss</i>	n.d.	AJ585760	CAE51384.1		
$\alpha$ -2,6-sialyltransferase (Siat1)	<i>Oncorhynchus mykiss</i>	n.d.	AJ620649	CAF05848.1		
$\alpha$ -2,8-polysialyltransferase IV (ST8Sia IV)	<i>Oncorhynchus mykiss</i>	n.d.	AB094402	BAC77411.1	Q7T2X5	
GalNAc $\alpha$ -2,6-sialyltransferase (RtST6GalNAc)	<i>Oncorhynchus mykiss</i>	n.d.	AB097943	BAC77520.1	Q7T2X4	
$\alpha$ -2,3-sialyltransferase ST3Gal IV	<i>Oryctolagus cuniculus</i>	2.4.99.-	AF121967	AAF28871.1	Q9N257	
OJ1217_F02.7	<i>Oryza sativa</i> (japonica cultivar-group)	n.d.	AP004084	BAD07616.1		
OSJNBa0043L24.2 or OSJNBb0002J11.9	<i>Oryza sativa</i> (japonica cultivar-group)	n.d.	AL731626 AL662969	CAD41185.1 CAE04714.1		
P0683f02.18 or P0489B03.1	<i>Oryza sativa</i> (japonica cultivar-group)	n.d.	AP003289 AP003794	BAB63715.1 BAB90552.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc V (Siat7E) (fragment)	<i>Oryzias latipes</i>	n.d.	AJ646876	CAG26705.1		
$\alpha$ -2,3-sialyltransferase ST3Gal I (Siat4)	<i>Pan troglodytes</i>	n.d.	AJ744803	CAG32839.1		
$\alpha$ -2,3-sialyltransferase ST3Gal II (Siat5)	<i>Pan troglodytes</i>	n.d.	AJ744804	CAG32840.1		
$\alpha$ -2,3-sialyltransferase ST3Gal III (Siat6)	<i>Pan troglodytes</i>	n.d.	AJ626819	CAF25177.1		
$\alpha$ -2,3-sialyltransferase ST3Gal IV (Siat4c)	<i>Pan troglodytes</i>	n.d.	AJ626824	CAF25182.1		
$\alpha$ -2,3-sialyltransferase ST3Gal VI (Siat10)	<i>Pan troglodytes</i>	n.d.	AJ744808	CAG32844.1		
$\alpha$ -2,6-sialyltransferase (Sia7A)	<i>Pan troglodytes</i>	n.d.	AJ748740	CAG38615.1		
$\alpha$ -2,6-sialyltransferase (Sia7B)	<i>Pan troglodytes</i>	n.d.	AJ748741	CAG38616.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc III (Siat7C)	<i>Pan troglodytes</i>	n.d.	AJ634454	CAG25676.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc IV (Siat7D) (fragment)	<i>Pan troglodytes</i>	n.d.	AJ646870	CAG26699.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc V (Siat7E)	<i>Pan troglodytes</i>	n.d.	AJ646875	CAG26704.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc VI (Siat7F) (fragment)	<i>Pan troglodytes</i>	n.d.	AJ646882	CAG26711.1		
$\alpha$ -2,8-sialyltransferase 8A (Siat8A)	<i>Pan troglodytes</i>	2.4.99.8	AJ697658	CAG26896.1		
$\alpha$ -2,8-sialyltransferase 8B (Siat8B)	<i>Pan troglodytes</i>	n.d.	AJ697659	CAG26897.1		
$\alpha$ -2,8-sialyltransferase 8C (Siat8C)	<i>Pan troglodytes</i>	n.d.	AJ697660	CAG26898.1		
$\alpha$ -2,8-sialyltransferase 8D (Siat8D)	<i>Pan troglodytes</i>	n.d.	AJ697661	CAG26899.1		
$\alpha$ -2,8-sialyltransferase	<i>Pan troglodytes</i>	n.d.	AJ697662	CAG26900.1		

FIGURE 9I

Protein	Organism	EC#	GenBank / GenPept		SwissProt	PDB / 3D
8E (Siat8E)						
$\alpha$ -2,8-sialyltransferase 8F (Siat8F)	<i>Pan troglodytes</i>	n.d.	AJ697663	CAG26901.1		
$\beta$ -galactosamide $\alpha$ -2,6-sialyltransferase I (ST6Gal I; Siat1)	<i>Pan troglodytes</i>	2.4.99.1	AJ627624	CAF29492.1		
$\beta$ -galactosamide $\alpha$ -2,6-sialyltransferase II (ST6Gal II)	<i>Pan troglodytes</i>	n.d.	AJ627625	CAF29493.1		
GM3 synthase ST3Gal V (Siat9)	<i>Pan troglodytes</i>	n.d.	AJ744807	CAG32843.1		
S138L	<i>Rabbit fibroma virus Kasza</i>	n.d.	NC_001266	NP_052025		
$\alpha$ -2,3-sialyltransferase ST3Gal III	<i>Rattus norvegicus</i>	2.4.99.6	M97754 NM_031697	AAA42146.1 NP_113885.1	Q02734	
$\alpha$ -2,3-sialyltransferase ST3Gal IV (Siat4c)	<i>Rattus norvegicus</i>	n.d.	AJ626825	CAF25183.1		
$\alpha$ -2,3-sialyltransferase ST3Gal VI	<i>Rattus norvegicus</i>	n.d.	AJ626743	CAF25053.1		
$\alpha$ -2,6-sialyltransferase ST3Gal II	<i>Rattus norvegicus</i>	2.4.99.-	X76988 NM_031695	CAA54293.1 NP_113883.1	Q11205	
$\alpha$ -2,6-sialyltransferase ST6Gal I	<i>Rattus norvegicus</i>	2.4.99.1	M18769 M83143	AAA41196.1 AAB07233.1	P13721	
$\alpha$ -2,6-sialyltransferase ST6GalNAc I (Siat7A)	<i>Rattus norvegicus</i>	n.d.	AJ634458	CAG25684.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc II (Siat7B)	<i>Rattus norvegicus</i>	n.d.	AJ634457	CAG25679.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc III	<i>Rattus norvegicus</i>	2.4.99.-	L29554 BC072501 NM_019123	AAC42086.1 AAH72501.1 NP_061996.1	Q64686	
$\alpha$ -2,6-sialyltransferase ST6GalNAc IV (Siat7D) (fragment)	<i>Rattus norvegicus</i>	n.d.	AJ646871	CAG26700.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc V (Siat7E)	<i>Rattus norvegicus</i>	n.d.	AJ646872	CAG26701.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc VI (Siat7F) (fragment)	<i>Rattus norvegicus</i>	n.d.	AJ646881	CAG26710.1		
$\alpha$ -2,8-sialyltransferase (GD3 synthase) ST8Sia I	<i>Rattus norvegicus</i>	2.4.99.-	U53883 D45255	AAC27541.1 BAA08213.1	P70554 P97713	
$\alpha$ -2,8-sialyltransferase (SIAT8E)	<i>Rattus norvegicus</i>	n.d.	AJ699422	CAG27884.1		
$\alpha$ -2,8-sialyltransferase (SIAT8F)	<i>Rattus norvegicus</i>	n.d.	AJ699423	CAG27885.1		
$\alpha$ -2,8-sialyltransferase ST8Sia II	<i>Rattus norvegicus</i>	2.4.99.-	L13445 NM_057156	AAA42147.1 NP_476497.1	Q07977 Q64688	
$\alpha$ -2,8-sialyltransferase ST8Sia III	<i>Rattus norvegicus</i>	2.4.99.-	U55938 NM_013029	AAB50061.1 NP_037161.1	P97877	
$\alpha$ -2,8-sialyltransferase ST8Sia IV	<i>Rattus norvegicus</i>	2.4.99.-	U90215	AAB49989.1	O08563	
$\beta$ -galactosamide $\alpha$ -2,6-sialyltransferase II (ST6Gal II)	<i>Rattus norvegicus</i>	n.d.	AJ627626	CAF29494.1		
GM3 synthase ST3Gal V	<i>Rattus norvegicus</i>	n.d.	AB018049 NM_031337	BAA33492.1 NP_112627.1	O88830	

FIGURE 9J

Protein	Organism	EC#	GenBank / GenPept		SwissProt	PDB / 3D
sialyltransferase ST3Gal-I (Siat4A)	<i>Rattus norvegicus</i>	n.d.	AJ748840	CAG44449.1		
$\alpha$ -2,3-sialyltransferase (ST3Gal-II)	<i>Silurana tropicalis</i>	n.d.	AJ585763	CAE51387.1		
$\alpha$ -2,6-sialyltransferase (Siat7b)	<i>Silurana tropicalis</i>	n.d.	AJ620650	CAF05849.1		
$\alpha$ -2,6-sialyltransferase (ST6galnac)	<i>Strongylocentrotus purpuratus</i>	n.d.	AJ699425	CAG27887.1		
$\alpha$ -2,3-sialyltransferase (ST3GAL-III)	<i>Sus scrofa</i>	n.d.	AJ585765	CAE51389.1		
$\alpha$ -2,3-sialyltransferase (ST3GAL-IV)	<i>Sus scrofa</i>	n.d.	AJ584674	CAE48299.1		
$\alpha$ -2,3-sialyltransferase ST3Gal I	<i>Sus scrofa</i>	2.4.99.4	M97753	AAA31125.1	Q02745	
$\alpha$ -2,6-sialyltransferase (fragment) ST6Gal I	<i>Sus scrofa</i>	2.4.99.1	AF136746	AAD33059.1	Q9XSG8	
$\beta$ -galactosamide $\alpha$ -2,6-sialyltransferase (ST6GalNAc-V)	<i>Sus scrofa</i>	n.d.	AJ620948	CAF06585.2		
sialyltransferase (fragment) ST6Gal I	<i>sus scrofa</i>	n.d.	AF041031	AAC15633.1	O62717	
ST6GALNAC-V	<i>Sus scrofa</i>	n.d.	AJ620948	CAF06585.1		
$\alpha$ -2,3-sialyltransferase (Siat5-r)	<i>Takifugu rubripes</i>	n.d.	AJ744805	CAG32841.1		
$\alpha$ -2,3-sialyltransferase ST3Gal I (Siat4)	<i>Takifugu rubripes</i>	n.d.	AJ626816	CAF25174.1		
$\alpha$ -2,3-sialyltransferase ST3Gal II (Siat5) (fragment)	<i>Takifugu rubripes</i>	n.d.	AJ626817	CAF25175.1		
$\alpha$ -2,3-sialyltransferase ST3Gal III (Siat6)	<i>Takifugu rubripes</i>	n.d.	AJ626818	CAF25176.1		
$\alpha$ -2,6-sialyltransferase ST6Gal I (Siat1)	<i>Takifugu rubripes</i>	n.d.	AJ744800	CAG32836.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc II (Siat7B)	<i>Takifugu rubripes</i>	n.d.	AJ634460	CAG25681.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc II B (Siat7B-related)	<i>Takifugu rubripes</i>	n.d.	AJ634461	CAG25682.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc III (Siat7C) (fragment)	<i>Takifugu rubripes</i>	n.d.	AJ634456	CAG25678.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc IV (siat7D) (fragment)	<i>Takifugu rubripes</i>	2.4.99.3	Y17466 AJ646869	CAB44338.1 CAG26698.1	Q9W6U6	
$\alpha$ -2,6-sialyltransferase ST6GalNAc V (Siat7E) (fragment)	<i>Takifugu rubripes</i>	n.d.	AJ646873	CAG26702.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc VI (Siat7F) (fragment)	<i>Takifugu rubripes</i>	n.d.	AJ646880	CAG26709.1		
$\alpha$ -2,8-sialyltransferase ST8Sia I (Siat 8A) (fragment)	<i>Takifugu rubripes</i>	n.d.	AJ715534	CAG29373.1		
$\alpha$ -2,8-sialyltransferase ST8Sia II (Siat 8B) (fragment)	<i>Takifugu rubripes</i>	n.d.	AJ715538	CAG29377.1		
$\alpha$ -2,8-sialyltransferase ST8Sia III (Siat 8C) (fragment)	<i>Takifugu rubripes</i>	n.d.	AJ715541	CAG29380.1		
$\alpha$ -2,8-sialyltransferase ST8Sia IIIr (Siat 8Cr)	<i>Takifugu rubripes</i>	n.d.	AJ715542	CAG29381.1		
$\alpha$ -2,8-sialyltransferase ST8Sia V (Siat 8E)	<i>Takifugu rubripes</i>	n.d.	AJ715547	CAG29386.1		

FIGURE 9K

Protein	Organism	EC#	GenBank / GenPept		SwissProt	PDB / 3D
(fragment)						
$\alpha$ -2,8-sialyltransferase ST8Sia VI (Siat 8F) (fragment)	<i>Takifugu rubripes</i>	n.d.	AJ715549	CAG29388.1		
$\alpha$ -2,8-sialyltransferase ST8Sia VIr (Siat 8Fr)	<i>Takifugu rubripes</i>	n.d.	AJ715550	CAG29389.1		
$\alpha$ -2,3-sialyltransferase (Siat5-r)	<i>Tetraodon nigroviridis</i>	n.d.	AJ744806	CAG32842.1		
$\alpha$ -2,3-sialyltransferase ST3Gal I (Siat4)	<i>Tetraodon nigroviridis</i>	n.d.	AJ744802	CAG32838.1		
$\alpha$ -2,3-sialyltransferase ST3Gal III (Siat6)	<i>Tetraodon nigroviridis</i>	n.d.	AJ626822	CAF25180.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc II (Siat7B)	<i>Tetraodon nigroviridis</i>	n.d.	AJ634462	CAG25683.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc V (Siat7E) (fragment)	<i>Tetraodon nigroviridis</i>	n.d.	AJ646879	CAG26708.1		
$\alpha$ -2,8-sialyltransferase ST8Sia I (Siat 8A) (fragment)	<i>Tetraodon nigroviridis</i>	n.d.	AJ715536	CAG29375.1		
$\alpha$ -2,8-sialyltransferase ST8Sia II (Siat 8B) (fragment)	<i>Tetraodon nigroviridis</i>	n.d.	AJ715537	CAG29376.1		
$\alpha$ -2,8-sialyltransferase ST8Sia III (Siat 8C) (fragment)	<i>Tetraodon nigroviridis</i>	n.d.	AJ715539	CAG29378.1		
$\alpha$ -2,8-sialyltransferase ST8Sia IIIr (Siat 8Cr) (fragment)	<i>Tetraodon nigroviridis</i>	n.d.	AJ715540	CAG29379.1		
$\alpha$ -2,8-sialyltransferase ST8Sia V (Siat 8E) (fragment)	<i>Tetraodon nigroviridis</i>	n.d.	AJ715548	CAG29387.1		
$\alpha$ -2,3-sialyltransferase (St3Gal-II)	<i>Xenopus laevis</i>	n.d.	AJ585762	CAE51386.1		
$\alpha$ -2,3-sialyltransferase (St3Gal-VI)	<i>Xenopus laevis</i>	n.d.	AJ585766	CAE51390.1		
$\alpha$ -2,3-sialyltransferase St3Gal-III (Siat6)	<i>Xenopus laevis</i>	n.d.	AJ585764 AJ626823	CAE51388.1 CAF25181.1		
$\alpha$ -2,8-polysialyltransferase	<i>Xenopus laevis</i>	2.4.99.-	AB007468	BAA32617.1	O93234	
$\alpha$ -2,8-sialyltransferase ST8Sia-I (Siat8A;GD3 synthase)	<i>Xenopus laevis</i>	n.d.	AY272056 AY272057 AJ704562	AAQ16162.1 AAQ16163.1 CAG28695.1		
Unknown (protein for MGC:81265)	<i>Xenopus laevis</i>	n.d.	BC068760	AAH68760.1		
$\alpha$ -2,3-sialyltransferase (3Gal-VI)	<i>Xenopus tropicalis</i>	n.d.	AJ626744	CAF25054.1		
$\alpha$ -2,3-sialyltransferase (Siat4c)	<i>Xenopus tropicalis</i>	n.d.	AJ622908	CAF22058.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc V (Siat7E) (fragment)	<i>Xenopus tropicalis</i>	n.d.	AJ646878	CAG26707.1		
$\alpha$ -2,8-sialyltransferase ST8Sia III (Siat 8C) (fragment)	<i>Xenopus tropicalis</i>	n.d.	AJ715544	CAG29383.1		
$\beta$ -galactosamide $\alpha$ -2,6-sialyltransferase II (ST6Gal II)	<i>Xenopus tropicalis</i>	n.d.	AJ627628	CAF29496.1		
sialyltransferase St8Sial	<i>Xenopus tropicalis</i>	n.d.	AY652775	AAT67042		
poly- $\alpha$ -2,8-sialosyl sialyltransferase (NeuS)	<i>Escherichia coli</i> K1	2.4.-.-	M76370 X60598	AAA24213.1 CAA43053.1	Q57269	
polysialyltransferase	<i>Escherichia coli</i> K92	2.4.-.-	M88479	AAA24215.1	Q47404	

FIGURE 9L

Protein	Organism	EC#	GenBank / GenPept		SwissProt	PDB / 3D
$\alpha$ -2,8 polysialyltransferase SiaD	<i>Neisseria meningitidis</i> B1940	2.4.-.-	M95053 X78068	AAA20478.1 CAA54985.1	Q51281 Q51145	
SynE	<i>Neisseria meningitidis</i> FAM18	n.d.	U75650	AAB53842.1	O06435	
polysialyltransferase (SiaD)(fragment)	<i>Neisseria meningitidis</i> M1019	n.d.	AY234192	AAO85290.1		
SiaD (fragment)	<i>Neisseria meningitidis</i> M209	n.d.	AY281046	AAP34769.1		
SiaD (fragment)	<i>Neisseria meningitidis</i> M3045	n.d.	AY281044	AAP34767.1		
polysialyltransferase (SiaD)(fragment)	<i>Neisseria meningitidis</i> M3315	n.d.	AY234191	AAO85289.1		
SiaD (fragment)	<i>Neisseria meningitidis</i> M3515	n.d.	AY281047	AAP34770.1		
polysialyltransferase (SiaD)(fragment)	<i>Neisseria meningitidis</i> M4211	n.d.	AY234190	AAO85288.1		
SiaD (fragment)	<i>Neisseria meningitidis</i> M4642	n.d.	AY281048	AAP34771.1		
polysialyltransferase (SiaD)(fragment)	<i>Neisseria meningitidis</i> M5177	n.d.	AY234193	AAO85291.1		
SiaD	<i>Neisseria meningitidis</i> M5178	n.d.	AY281043	AAP34766.1		
SiaD (fragment)	<i>Neisseria meningitidis</i> M980	n.d.	AY281045	AAP34768.1		
NMB0067	<i>Neisseria meningitidis</i> MC58	n.d.	NC_003112	NP_273131		
Lst	<i>Aeromonas punctata</i> Sch3	n.d.	AF126256	AAS66624.1		
ORF2	<i>Haemophilus influenzae</i> A2	n.d.	M94855	AAA24979.1		
HI1699	<i>Haemophilus influenzae</i> Rd	n.d.	U32842 NC_000907	AAC23345.1 NP_439841.1	Q48211	
$\alpha$ -2,3-sialyltransferase	<i>Neisseria gonorrhoeae</i> F62	2.4.99.4	U60664	AAC44539.1 AAE67205.1	P72074	
$\alpha$ -2,3-sialyltransferase	<i>Neisseria meningitidis</i> 126E, NRCC 4010	2.4.99.4	U60662	AAC44544.2		
$\alpha$ -2,3-sialyltransferase	<i>Neisseria meningitidis</i> 406Y, NRCC 4030	2.4.99.4	U60661	AAC44543.1		
$\alpha$ -2,3-sialyltransferase (NMB0922)	<i>Neisseria meningitidis</i> MC58	2.4.99.4	U60660 AE002443 NC_003112	AAC44541.1 AAF41330.1 NP_273962.1	P72097	
NMA1118	<i>Neisseria meningitidis</i> Z2491	n.d.	AL162755 NC_003116	CAB84380.1 NP_283887.1	Q9JUV5	
PM0508	<i>Pasteurella multocida</i> PM70	n.d.	AE006086 NC_002663	AAK02592.1 NP_245445.1	Q9CNC4	
WaaH	<i>Salmonella enterica</i> SARB25	n.d.	AF519787	AAM82550.1	Q8KS93	
WaaH	<i>Salmonella enterica</i> SARB3	n.d.	AF519788	AAM82551.1	Q8KS92	
WaaH	<i>Salmonella enterica</i> SARB39	n.d.	AF519789	AAM82552.1		
WaaH	<i>Salmonella enterica</i> SARB53	n.d.	AF519790	AAM82553.1		
WaaH	<i>Salmonella enterica</i> SARB57	n.d.	AF519791	AAM82554.1	Q8KS91	
WaaH	<i>Salmonella enterica</i> SARB71	n.d.	AF519793	AAM82556.1	Q8KS89	
WaaH	<i>Salmonella enterica</i>	n.d.	AF519792	AAM82555.1	Q8KS90	

FIGURE 9M

Protein	Organism	EC#	GenBank / GenPept		SwissProt	PDB / 3D
	<b>SARB8</b>					
WaaH	<i>Salmonella enterica</i> SARC10V	n.d.	AF519779	AAM88840.1	Q8KS99	
WaaH (fragment)	<i>Salmonella enterica</i> SARC12	n.d.	AF519781	AAM88842.1		
WaaH (fragment)	<i>Salmonella enterica</i> SARC13I	n.d.	AF519782	AAM88843.1	Q8KS98	
WaaH (fragment)	<i>Salmonella enterica</i> SARC14I	n.d.	AF519783	AAM88844.1	Q8KS97	
WaaH	<i>Salmonella enterica</i> SARC15II	n.d.	AF519784	AAM88845.1	Q8KS96	
WaaH	<i>Salmonella enterica</i> SARC16II	n.d.	AF519785	AAM88846.1	Q8KS95	
WaaH (fragment)	<i>Salmonella enterica</i> SARC3I	n.d.	AF519772	AAM88834.1	Q8KSA4	
WaaH (fragment)	<i>Salmonella enterica</i> SARC4I	n.d.	AF519773	AAM88835.1	Q8KSA3	
WaaH	<i>Salmonella enterica</i> SARC5IIa	n.d.	AF519774	AAM88836.1		
WaaH	<i>Salmonella enterica</i> SARC6IIa	n.d.	AF519775	AAM88837.1	Q8KSA2	
WaaH	<i>Salmonella enterica</i> SARC8	n.d.	AF519777	AAM88838.1	Q8KSA1	
WaaH	<i>Salmonella enterica</i> SARC9V	n.d.	AF519778	AAM88839.1	Q8KSA0	
UDP-glucose : $\alpha$ -1,2-glucosyltransferase (WaaH)	<i>Salmonella enterica</i> subsp. <i>arizonae</i> SARC 5	2.4.1.-	AF511116	AAM48166.1		
bifunctional $\alpha$ -2,3/-2,8-sialyltransferase (Cst-II)	<i>Campylobacter jejuni</i> ATCC 43449	n.d.	AF401529	AAL06004.1	Q93CZ5	
Cst	<i>Campylobacter jejuni</i> 81-176	n.d.	AF305571	AAL09368.1		
$\alpha$ -2,3-sialyltransferase (Cst-III)	<i>Campylobacter jejuni</i> ATCC 43429	2.4.99.-	AY044156	AAK73183.1		
$\alpha$ -2,3-sialyltransferase (Cst-III)	<i>Campylobacter jejuni</i> ATCC 43430	2.4.99.-	AF400047	AAK85419.1		
$\alpha$ -2,3-sialyltransferase (Cst-II)	<i>Campylobacter jejuni</i> ATCC 43432	2.4.99.-	AF215659	AAG43979.1	Q9F0M9	
$\alpha$ -2,3/8-sialyltransferase (CstII)	<i>Campylobacter jejuni</i> ATCC 43438	n.d.	AF400048	AAK91725.1	Q93MQ0	
$\alpha$ -2,3-sialyltransferase cst-II	<i>Campylobacter jejuni</i> ATCC 43446	2.4.99.-	AF167344	AAF34137.1		
$\alpha$ -2,3-sialyltransferase (Cst-II)	<i>Campylobacter jejuni</i> ATCC 43456	2.4.99.-	AF401528	AAL05990.1	Q93D05	
$\alpha$ -2,3/- $\alpha$ -2,8-sialyltransferase (CstII)	<i>Campylobacter jejuni</i> ATCC 43460	2.4.99.-	AY044868	AAK96001.1	Q938X6	
$\alpha$ -2,3/8-sialyltransferase (Cst-II)	<i>Campylobacter jejuni</i> ATCC 700297	n.d.	AF216647	AAL36462.1		
ORF	<i>Campylobacter jejuni</i> GB11	n.d.	AY422197	AAR82875.1		
$\alpha$ -2,3-sialyltransferase cstIII	<i>Campylobacter jejuni</i> MSC57360	2.4.99.-	AF195055	AAG29922.1		
$\alpha$ -2,3-sialyltransferase cstIII Cj1140	<i>Campylobacter jejuni</i> NCTC 11168	2.4.99.-	AL139077 NC_002163	CAB73395.1 NP_282288.1	Q9PNF4	
$\alpha$ -2,3/ $\alpha$ -2,8-sialyltransferase II (cstII)	<i>Campylobacter jejuni</i> O:10	n.d.	- AX934427	AAO96669.1 CAF04167.1		
$\alpha$ -2,3/ $\alpha$ -2,8-sialyltransferase II (CstII)	<i>Campylobacter jejuni</i> O:19	n.d.	AX934431	CAF04169.1		
$\alpha$ -2,3/ $\alpha$ -2,8-sialyltransferase II (CstII)	<i>Campylobacter jejuni</i> O:36	n.d.	AX934436	CAF04171.1		
$\alpha$ -2,3/ $\alpha$ -2,8-	<i>Campylobacter</i>	n.d.	AX934434	CAF04170.1		

FIGURE 9N

Protein	Organism	EC#	GenBank / GenPept		SwissProt	PDB / 3D
sialyltransferase II (CstII)	<i>jejuni</i> O:4					
$\alpha$ -2,3/ $\alpha$ -2,8-sialyltransferase II (CstII)	<i>Campylobacter jejuni</i> O:41	n.d.	-	AAO96670.1 AAT17967.1 CAF04168.1		
$\alpha$ -2,3-sialyltransferase cst-I	<i>Campylobacter jejuni</i> OH4384	2.4.99.-	AF130466 -	AAF13495.1 AAS36261.1	Q9RGF1	
bifunctional $\alpha$ -2,3/-2,8-sialyltransferase (Cst-II)	<i>Campylobacter jejuni</i> OH4384	2.4.99.-	AF130984 AX934425	AAF31771.1 CAF04166.1	1RO7 1RO8	C A
HI0352 (fragment)	<i>Haemophilus influenzae</i> Rd	n.d.	U32720 X57315 NC_000907	AAC22013.1 CAA40567.1 NP_438516.1	P24324	
PM1174	<i>Pasteurella multocida</i> PM70	n.d.	AE006157 NC_002663	AAK03258.1 NP_246111.1	Q9CLP3	
Sequence 10 from patent US 6503744	Unknown.	n.d.	-	AAO96672.1		
Sequence 10 from patent US 6699705	Unknown.	n.d.	-	AAT17969.1		
Sequence 12 from patent US 6699705	Unknown.	n.d.	-	AAT17970.1		
Sequence 2 from patent US 6709834	Unknown.	n.d.	-	AAT23232.1		
Sequence 3 from patent US 6503744	Unknown.	n.d.	-	AAO96668.1		
Sequence 3 from patent US 6699705	Unknown.	n.d.	-	AAT17965.1		
Sequence 34 from patent US 6503744	Unknown.	n.d.	-	AAO96684.1		
Sequence 35 from patent US 6503744 (fragment)	Unknown.	n.d.	-	AAO96685.1 AAS36262.1		
Sequence 48 from patent US 6699705	Unknown.	n.d.	-	AAT17988.1		
Sequence 5 from patent US 6699705	Unknown.	n.d.	-	AAT17966.1		
Sequence 9 from patent US 6503744	Unknown.	n.d.	-	AAO96671.1		